

Serial Number: 09/229,751A

**ENTERED**

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was  the prior application data; or  other \_\_\_\_\_

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

79

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:

**RECEIVED**

DEC 1 1 2000

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted:  non-ASCII "garbage" at the beginning/end of files;  secretary initials/filename at end of file;  
 page numbers throughout text;  other invalid text, such as \_\_\_\_\_

Inserted mandatory headings, specifically: \_\_\_\_\_

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_

Other:

**Examiner:** The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING DATE: 11/27/2000  
PATENT APPLICATION: US/09/229,751A TIME: 17:42:32

Input Set : A:\PTO.txt  
Output Set: N:\CRF3\11272000\I229751A.raw

Does Not Comply  
Corrected Diskette Needed

**SEQUENCE LISTING**



ERRORRED SEQUENCES

- 64 (2) INFORMATION FOR SEQ ID NO: 2:  
65 (i) SEQUENCE CHARACTERISTICS:  
66 (A) LENGTH: 21 base pairs  
67 (B) TYPE: nucleic acid  
68 (C) STRANDEDNESS: single  
69 (D) TOPOLOGY: unknown  
70 (ii) MOLECULE TYPE: DNA (genomic)  
71 (iii) HYPOTHETICAL: NO  
72 (iv) ANTI-SENSE: NO  
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
E--> 82 AATCATTTTT TGATTAAGCC G  
W--> 83 21  
85 (2) INFORMATION FOR SEQ ID NO: 3:

RAW SEQUENCE LISTING  
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87      (i) SEQUENCE CHARACTERISTICS:
88          (A) LENGTH: 21 base pairs
89          (B) TYPE: nucleic acid
90          (C) STRANDEDNESS: single
91          (D) TOPOLOGY: unknown
93      (ii) MOLECULE TYPE: DNA (genomic)
95      (iii) HYPOTHETICAL: NO
97      (iv) ANTI-SENSE: NO
101      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 103 AATCATTTC TGAGGTCTCC G
W--> 104 21
127 (2) INFORMATION FOR SEQ ID NO: 5:
129      (i) SEQUENCE CHARACTERISTICS:
130          (A) LENGTH: 21 base pairs
131          (B) TYPE: nucleic acid
132          (C) STRANDEDNESS: single
133          (D) TOPOLOGY: unknown
135      (ii) MOLECULE TYPE: DNA (genomic)
137      (iii) HYPOTHETICAL: NO
139      (iv) ANTI-SENSE: NO
143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
E--> 145 AATCATTTTC TTCCTTAAGGT G
W--> 146 21
148 (2) INFORMATION FOR SEQ ID NO: 6:
150      (i) SEQUENCE CHARACTERISTICS:
151          (A) LENGTH: 21 base pairs
152          (B) TYPE: nucleic acid
153          (C) STRANDEDNESS: single
154          (D) TOPOLOGY: unknown
156      (ii) MOLECULE TYPE: DNA (genomic)
158      (iii) HYPOTHETICAL: NO
160      (iv) ANTI-SENSE: NO
164      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
E--> 166 AATCATTTTC TGTTGCCGCC G
W--> 167 21
169 (2) INFORMATION FOR SEQ ID NO: 7:
171      (i) SEQUENCE CHARACTERISTICS:
172          (A) LENGTH: 21 base pairs
173          (B) TYPE: nucleic acid
174          (C) STRANDEDNESS: single
175          (D) TOPOLOGY: unknown
177      (ii) MOLECULE TYPE: peptide
179      (iii) HYPOTHETICAL: NO
181      (iv) ANTI-SENSE: NO
185      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
E--> 187 AATCATTTTC TGCCTCGTTG G
W--> 188 21
190 (2) INFORMATION FOR SEQ ID NO: 8:
192      (i) SEQUENCE CHARACTERISTICS:

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*same*

*error*

RAW SEQUENCE LISTING  
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Input Set : A:\PTO.txt  
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193 (A) LENGTH: 21 base pairs  
194 (B) TYPE: nucleic acid  
195 (C) STRANDEDNESS: single  
196 (D) TOPOLOGY: unknown  
198 (ii) MOLECULE TYPE: peptide  
200 (iii) HYPOTHETICAL: NO  
202 (iv) ANTI-SENSE: NO  
206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
E--> 208 AATCATTTT TGCCCTCTCG G  
W--> 209 21  
211 (2) INFORMATION FOR SEQ ID NO: 9:  
213 (i) SEQUENCE CHARACTERISTICS:  
214 (A) LENGTH: 21 base pairs  
215 (B) TYPE: nucleic acid  
216 (C) STRANDEDNESS: single  
217 (D) TOPOLOGY: unknown  
219 (ii) MOLECULE TYPE: DNA (genomic)  
221 (iii) HYPOTHETICAL: NO  
223 (iv) ANTI-SENSE: NO  
227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
E--> 229 AATCATTTC TGATGCCGAA G  
W--> 230 21  
232 (2) INFORMATION FOR SEQ ID NO: 10:  
234 (i) SEQUENCE CHARACTERISTICS:  
235 (A) LENGTH: 21 base pairs  
236 (B) TYPE: nucleic acid  
237 (C) STRANDEDNESS: single  
238 (D) TOPOLOGY: unknown  
240 (ii) MOLECULE TYPE: DNA (genomic)  
242 (iii) HYPOTHETICAL: NO  
244 (iv) ANTI-SENSE: NO  
248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
E--> 250 AATCATTTC TGCCTACTGG G  
W--> 251 21  
253 (2) INFORMATION FOR SEQ ID NO: 11:  
255 (i) SEQUENCE CHARACTERISTICS:  
256 (A) LENGTH: 21 base pairs  
257 (B) TYPE: nucleic acid  
258 (C) STRANDEDNESS: single  
259 (D) TOPOLOGY: unknown  
261 (ii) MOLECULE TYPE: DNA (genomic)  
263 (iii) HYPOTHETICAL: NO  
265 (iv) ANTI-SENSE: NO  
269 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
E--> 271 AATCATTTC TTAAGGGGAC G  
W--> 272 21  
274 (2) INFORMATION FOR SEQ ID NO: 12:  
276 (i) SEQUENCE CHARACTERISTICS:  
277 (A) LENGTH: 21 base pairs

*same*

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Input Set : A:\PTO.txt  
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278 (B) TYPE: nucleic acid  
279 (C) STRANDEDNESS: single  
280 (D) TOPOLOGY: unknown  
282 (ii) MOLECULE TYPE: DNA (genomic)  
284 (iii) HYPOTHETICAL: NO  
286 (iv) ANTI-SENSE: NO  
290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
E--> 292 ATTCAATTTC TTCTTTGGCG T  
W--> 293 21  
295 (2) INFORMATION FOR SEQ ID NO: 13:  
297 (i) SEQUENCE CHARACTERISTICS:  
298 (A) LENGTH: 21 base pairs  
299 (B) TYPE: nucleic acid  
300 (C) STRANDEDNESS: single  
301 (D) TOPOLOGY: unknown  
303 (ii) MOLECULE TYPE: DNA (genomic)  
305 (iii) HYPOTHETICAL: NO  
307 (iv) ANTI-SENSE: NO  
311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
E--> 313 AATCAATTTC TGATTAGGAA G  
W--> 314 21  
316 (2) INFORMATION FOR SEQ ID NO: 14:  
318 (i) SEQUENCE CHARACTERISTICS:  
319 (A) LENGTH: 21 base pairs  
320 (B) TYPE: nucleic acid  
321 (C) STRANDEDNESS: single  
322 (D) TOPOLOGY: unknown  
324 (ii) MOLECULE TYPE: DNA (genomic)  
326 (iii) HYPOTHETICAL: NO  
328 (iv) ANTI-SENSE: NO  
332 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
E--> 334 AATCAATTTC TGCCGACTGC T  
W--> 335 21  
379 (2) INFORMATION FOR SEQ ID NO: 17:  
381 (i) SEQUENCE CHARACTERISTICS:  
382 (A) LENGTH: 21 base pairs  
383 (B) TYPE: nucleic acid  
384 (C) STRANDEDNESS: single  
385 (D) TOPOLOGY: unknown  
387 (ii) MOLECULE TYPE: DNA (genomic)  
389 (iii) HYPOTHETICAL: NO  
391 (iv) ANTI-SENSE: NO  
395 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
E--> 397 ATTCAATTTC TGCCGCAGAA T  
W--> 398 21  
989 (2) INFORMATION FOR SEQ ID NO: 46:  
991 (i) SEQUENCE CHARACTERISTICS:  
992 (A) LENGTH: 21 base pairs  
993 (B) TYPE: nucleic acid



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994      (C) STRANDEDNESS: single
995      (D) TOPOLOGY: unknown
997      (ii) MOLECULE TYPE: DNA (genomic)
999      (iii) HYPOTHETICAL: NO
1001      (iv) ANTI-SENSE: NO
1005      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
E--> 1007 ACGCATCGTT TGCCTTCTCG G
W--> 1008 21
1010 (2) INFORMATION FOR SEQ ID NO: 47:
1012      (i) SEQUENCE CHARACTERISTICS:
1013          (A) LENGTH: 21 base pairs
1014          (B) TYPE: nucleic acid
1015          (C) STRANDEDNESS: single
1016          (D) TOPOLOGY: unknown
1018      (iii) MOLECULE TYPE: DNA (genomic)
1020      (iii) HYPOTHETICAL: NO
1022      (iv) ANTI-SENSE: NO
1026      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
E--> 1028 GTTACTAGTA GGGGAAATGT T
W--> 1029 21
1031 (2) INFORMATION FOR SEQ ID NO: 48:
1033      (i) SEQUENCE CHARACTERISTICS:
1034          (A) LENGTH: 21 base pairs
1035          (B) TYPE: nucleic acid
1036          (C) STRANDEDNESS: single
1037          (D) TOPOLOGY: unknown
1039      (ii) MOLECULE TYPE: DNA (genomic)
1041      (iii) HYPOTHETICAL: NO
1043      (iv) ANTI-SENSE: NO
1047      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
E--> 1049 AAGCTGTGGG TGATTCCTCA G
W--> 1050 21
1052 (2) INFORMATION FOR SEQ ID NO: 49:
1054      (i) SEQUENCE CHARACTERISTICS:
1055          (A) LENGTH: 21 base pairs
1056          (B) TYPE: nucleic acid
1057          (C) STRANDEDNESS: single
1058          (D) TOPOLOGY: unknown
1060      (ii) MOLECULE TYPE: DNA (genomic)
1062      (iii) HYPOTHETICAL: NO
1064      (iv) ANTI-SENSE: NO
1068      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:
E--> 1070 TATTCGCCCTC CTCATAGGCA T
W--> 1071 21
1220 (2) INFORMATION FOR SEQ ID NO: 57:
1222      (i) SEQUENCE CHARACTERISTICS:
1223          (A) LENGTH: 21 base pairs
1224          (B) TYPE: nucleic acid
1225          (C) STRANDEDNESS: single

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Input Set : A:\PTO.txt  
Output Set: N:\CRF3\11272000\I229751A.raw

1226 (D) TOPOLOGY: unknown  
 1228 (ii) MOLECULE TYPE: DNA (genomic)  
 1230 (iii) HYPOTHETICAL: NO  
 1232 (iv) ANTI-SENSE: NO  
 1236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
 E--> 1238 TCGTATCCTC CGTATTTGA T  
 W--> 1239 21  
 1241 (2) INFORMATION FOR SEQ ID NO: 58:  
 1243 (i) SEQUENCE CHARACTERISTICS:  
 1244 (A) LENGTH: 21 base pairs  
 1245 (B) TYPE: nucleic acid  
 1246 (C) STRANDEDNESS: single  
 1247 (D) TOPOLOGY: unknown  
 1249 (ii) MOLECULE TYPE: DNA (genomic)  
 1251 (iii) HYPOTHETICAL: NO  
 1253 (iv) ANTI-SENSE: NO  
 1257 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
 E--> 1259 CTTTTGTCGC CTCTGCATCG T  
 W--> 1260 21  
 1262 (2) INFORMATION FOR SEQ ID NO: 59:  
 1264 (i) SEQUENCE CHARACTERISTICS:  
 1265 (A) LENGTH: 21 base pairs  
 1266 (B) TYPE: nucleic acid  
 1267 (C) STRANDEDNESS: single  
 1268 (D) TOPOLOGY: unknown  
 1270 (ii) MOLECULE TYPE: DNA (genomic)  
 1272 (iii) HYPOTHETICAL: NO  
 1274 (iv) ANTI-SENSE: NO  
 1278 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
 E--> 1280 TTTGATTCCTC CGCTTCGTCG G  
 W--> 1281 21  
 1662 (2) INFORMATION FOR SEQ ID NO: 78:  
 1664 (i) SEQUENCE CHARACTERISTICS:  
 1665 (A) LENGTH: 7 amino acids  
 1666 (B) TYPE: amino acid  
 1667 (C) STRANDEDNESS: single  
 1668 (D) TOPOLOGY: unknown  
 1670 (ii) MOLECULE TYPE: peptide  
 1572 (iii) HYPOTHETICAL: NO  
 1674 (iv) ANTI-SENSE: NO  
 1678 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:  
 1680 Phe Asp Ser Pro Leu Arg Arg  
 1681 1 5  
 1683 (2) INFORMATION FOR SEQ ID NO: 78:  
 1685 (i) SEQUENCE CHARACTERISTICS:  
 1686 (A) LENGTH: 7 amino acids  
 1687 (B) TYPE: amino acid  
 1688 (C) STRANDEDNESS: single  
 1689 (D) TOPOLOGY: unknown

*Same*

RAW SEQUENCE LISTING  
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Input Set : A:\PTO.txt  
Output Set: N:\CRF3\11272000\I229751A.raw

1691 (iii) MOLECULE TYPE: peptide  
1693 (iii) HYPOTHETICAL: NO  
1695 (iv) ANTI-SENSE: NO  
E--> 1699 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79  
1701 Trp Ser Pro Leu His Lys His  
1702 1 5  
E--> 1704 (2) INFORMATION FOR SEQ ID NO: 80:  
1706 (i) SEQUENCE CHARACTERISTICS:  
1707 (A) LENGTH: 12 amino acids  
1708 (B) TYPE: amino acid  
1709 (C) STRANDEDNESS: single  
1710 (D) TOPOLOGY: unknown  
1712 (ii) MOLECULE TYPE: peptide  
1714 (iii) HYPOTHETICAL: NO  
1715 (iv) ANTI-SENSE: NO  
1720 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:  
1722 Asn His Phe Leu Lys Ser Gln Pro Gly Val Val Thr  
1723 1 5 10

OK

VERIFICATION SUMMARY DATE: 11/27/2000  
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Input Set : A:\PTO.txt  
Output Set: N:\CRF3\11272000\I229751A.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:82 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:2  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:103 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:3  
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:145 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:5  
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:166 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:6  
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
L:187 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:7  
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:208 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:8  
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8  
L:229 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:9  
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:250 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:10  
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:271 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:11  
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:292 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:12  
L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:313 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:13  
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:334 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:14  
L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14  
L:397 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:17  
L:398 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:1007 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:46  
L:1008 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46  
L:1028 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:47  
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:47  
L:1049 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:48  
L:1050 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:48  
L:1070 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:49  
L:1071 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49  
L:1238 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:57  
L:1239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:57  
L:1259 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:58  
L:1260 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:58  
L:1280 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:59  
L:1281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:59  
L:1301 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:60  
L:1302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:60  
L:1322 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:61  
L:1323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:61  
L:1343 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:62  
L:1344 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:62

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Input Set : A:\PTO.txt  
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L:1364 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:63  
L:1365 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:63  
L:1385 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:64  
L:1386 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:64  
L:1406 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:65  
L:1407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:65  
L:1427 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:66  
L:1428 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:66  
L:1449 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:67  
L:1450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:67  
L:1470 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:68  
L:1471 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:68  
L:1491 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:69  
L:1492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:69  
L:1512 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:70  
L:1513 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70  
L:1533 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:71  
L:1534 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:71  
L:1699 M:212 E: (34) Invalid or duplicate Sequence ID Number, Data=[79:]  
L:1704 M:216 E: (34) Seq.#s missing, 81 thru 79